CRTC

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: _DAVID GUZO_ Examiner # : _70677_ Date: _7/10/06_

Art Unit: _1636_ Phone Number: _2-0767_ Serial Number: _10/765,456_

Location (Bldg/Room#): _Remsen 2A79_ (Mailbox #): _2C70_ Results Format Preferred (circle): (PAPER) DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Date: _____

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please run a regular plus interference sequence search on SEQ ID NO: 1 and 3.

seq 1 - 521AA
seq 3 - 1584NA

Thanks

GenCore version 5.1.9
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QM protein - protein search, using sw model

Run on: July 11, 2006, 08:30:11 ; Search time 41 Seconds
                (without alignments)
                1236.737 Million cell updates/sec

Title: US-10-765-456-1
Perfect score: 2790
Sequence: 1 MNQISKNDSLDVLQDEMGQK.........YWEIMQFHNLKRQQLRAIIE 527
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_80:*
           1: pir1:*
           2: pir2:*
           3: pir3:*
           4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	244.5	8.8	710	2	T50469	hypothetical prote
2	244.5	8.8	710	2	A25657	hypothetical prote
3	244.5	8.8	720	2	T50475	hypothetical prote
4	213	7.6	470	2	E97331	reverse transcript
5	205.5	7.4	418	2	H83677	reverse transcript
6	204.5	6.4	418	2	G83654	transpose (11) B
7	178.5	6.4	599	2	S77648	transpose (11) B
8	171.5	6.1	453	2	A95946	maturase-related p
9	166.5	6.0	790	2	E48327	probable reverse t
10	163.5	6.0	392	2	G96004	COI intron A prote
11	161	5.8	574	2	C96004	probable reverse t
12	157	5.6	788	2	T00245	reverse transcript
13	156.5	5.6	318	2	B48327	COI intron alpha-s
14	155	5.6	602	2	S58503	reverse transcript
15	155	5.5	461	2	G59091	hypothetical prote
16	154	5.5	668	2	G59093	hypothetical prote
17	154	5.5	1260	4	AG1989	retrovirus-related
18	154	5.5	368	2	GNLRL1	hypothetical prote
19	153	5.5	633	2	S01651	retrovirus-related
20	151	5.4	1084	2	T31160	probable RNA-direc
21	151	5.3	608	2	T31173	maturase-related p
22	148.5	5.3	608	2	S05341	RNA-directed DNA p
23	146.5	5.3	308	2	S58504	probable reverse t
24	146	5.2	785	2	S63652	reverse transcript
25	146	5.2	308	2	QXBY31	hypothetical prote
26	144	5.2	834	1	S78642	gene coxI intron 1
27	141	5.1	834	2	S50828	gene coxI intron 1
28	141	5.0	416	2	QXBY31	hypothetical prote
29	138.5	4.9	1352	2	G84473	hypothetical prote
28	137	4.9	330	2	E98119	transpoease, uncha
29	136	4.9	860	2	S55543	RNA-directed DNA p
30	134.5	4.8	376	2	B64751	ykfC protein - Esc
31	134.5	4.8	546	2	T11217	reverse transcript
32	133	4.8	571	2	T31170	maturase-related p
33	132.5	4.7	544	2	T11216	reverse transcript
34	131	4.7	1259	4	GNHU1	retrovirus-related
35	131	4.7	1275	2	S65824	reverse transcript
36	131	4.6	908	2	S07649	gene coi intron 1
37	130	4.6	1045	2	S23570	hypothetical prote
38	127	4.6	1280	2	B34087	pol polyprotein ho
39	127	4.6	502	2	S26004	18S rRNA intron 1
40	124.5	4.5	600	2	AE2570	hypothetical prote
41	124.5	4.5	1226	2	H64479	protoporphyrin IX
42	123.5	4.5	1258	2	T14853	reverse transcript
43	120.5	4.3	827	2	S25949	gene coxII intron
44	120.5	4.3	1224	2	S25952	gene cob intron 3
45	120.5	4.3	2517	2	S58380	probable RNA-direc

ALIGNMENTS

RESULT 1
T50469
hypothetical protein [imported] - Neurospora crassa mitochondrion plasmid Varkud
C;Species: mitochondrion Neurospora crassa
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
R;Akins, R.A.; Grant, D.M.; Stohl, L.L.; Boctorff, D.A.; Nargang, F.E.; Lambowitz, A.M.
J. Mol. Biol. 204, 1-25, 1988
A;Title: Nucleotide sequence of the Varkud mitochondrial plasmid of Neurospora and synt
A;Reference number: Z25078; MUID:89110991; PMID:3216387
A;Accession: T50469
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-710 <AKI>
A;Cross-references: UNIPROT:O35156; UNIPARC:UPI00000925A5; EMBL:X13801; NID:g2941; PID
A;Genetics:
A;Genome: mitochondrion plasmid Varkud
A;Genetic code: SGC3
A;Introns: 30/3
C;Keywords: mitochondrion

Query Match   8.8%;
Best Local Similarity 25.4%;
Matches   95; Conservative   61; Mismatches 151; Indels   67; Gaps   13;

Score 244.5; DB 2; Length 710;
Pred. No. 2.4e-09;

```
Qy    1 MNQISKNDSLDVLQDEMGQKKTFESERKSLSGWDYFKSLGSIGRLPHFSRGIELREVKKA 60
          ::    :  :  :   : :::   :    :    ::   ::   : ::   :
Db   10 VSYIGENHELSWLHGMFGLLKRSNPQIGGMLGW------------------LNTG------ 47

Qy   61 NRYLAFQEQRIVSAIEAGEIRKAVLVWLCLMKVSRSYQILLFNRVCKGWYWRNSTARVEE 120
         :   :   :  :: : : :: : :  ::   :  :   :::::::::: ::  :::: ::
Db   48 NGFVKYMMNLMGHARDKGDAKEYWRLGRSLMK-NEAFQVQAFNHVCKHWYLDYKPHKIAK 106

Qy  121 IIFGAMNKMRSWDMKLLIHRFYILLKKNGKMRPIGAPNYESRMISKALTDML--YSITEKS 178
         ::  :     :   :::::: ::: ::::::::::  :: :  :::      :   :
Db  107 LLKEVREMVELQPVCIDYKRVVIPKANGKQRPLGVPTVPWRVYLHMNNVLLVWYRIPEQD 166

Qy  179 RSAEQHGYMKKRGAWSAILECLSKLKEGYAGYEFDLKSFNTVEPFIYFRKLEE--VDKK 236
          :  :  : :::  :  :   :  :   :  :::::::: : :::::::::: ::  ::
Db  167 ---NQHAYFPKRGVFTAWRALWPKLL-DSQNIYEFDLKNFPPSVDLAYLKDRLMESGIPQD 222

Qy  237 LTKLIISNVIKGIEYRFSE-LLPE-------SELNPKANRKNTLE-------------- 272
          ::     :     :   : :::           :::::: :::
Db  223 ISEYLTVIARSLVLVLTSEDKIPEPHRDVIFNSDGTPNPNLPKDVQGRIILKDPFVEILRR 282

Qy  273 ------RTGVPQGLSLSPLLSTWAL-EYYGRPENLIMYIADDGIYFFKHNISKFTRWIER 324
              :::::::: : ::::: :  :::::::::::::::::
Db  283 RGFTDIATNGVPQGASTSCGLATYNVKELFKRYDELIMYADDGI-LCRQDPSTPDFSIE- 340

Qy  325 MGRAGIEISPEKSG 338
          ::| :|:| ||||
Db  341 --EAGVVQEPAKSG 352
```

OM protein - protein search, using sw model

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Run on: July 11, 2006, 08:26:50 ; Search time 300 Seconds ,
(without alignments)
1624.944 Million cell updates/sec

```
Title:          US-10-765-456-1
Perfect score:  2790
Sequence:       1 MNQISKNDSLDVLQDEMGQOK........YWEIMQFHNLKRQQLRAIIE 527

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:  2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  UniProt_7.2:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2790	100.0	527	2	Q9XNK5_FUSOX	fusarium ox
2	2550	91.4	527	2	Q9XNK4_FUSOX	fusarium ox
3	2052	73.5	397	2	O21164_FUSOX	fusarium ox
4	420	15.1	262	2	O21165_FUSOX	fusarium ox
5	315	11.3	605	2	Q9MEH5_TRIHA	trichoderma
6	270.5	9.7	294	2	Q9XMG3_EPITY	epichloe ty
7	245.5	8.8	710	2	Q59Q1_NEUIN	neurospora
8	245	8.8	710	2	Q59Q0_NEUIN	neurospora
9	244.5	8.8	710	2	Q7GEY3_NEUCR	neurospora
10	244.5	8.8	720	2	Q35156_NEUIN	neurospora
11	243.5	8.7	710	2	Q36578_NEUIN	neurospora
12	243.5	8.7	710	2	Q36578_NEUIN	neurospora
13	227.5	8.2	439	2	Q3C244_STRAG	streptococc
14	227.5	8.2	439	2	Q8E028_STRA5	streptococc
15	220	7.9	482	2	Q3GD28_9FIRM	syntrophomo
16	219.5	7.9	433	2	Q2WLJ7_CLOBE	clostridium
17	216.5	7.8	470	2	Q3CK71_THEET	thermoanaer
18	216.5	7.8	470	2	Q3CK71_THEET	thermoanaer
19	214.5	7.7	462	2	Q93PB4_9SPHI	microscilla
20	214	7.7	470	2	Q3CJ27_THEET	thermoanaer
21	213.5	7.7	470	2	Q3CES5_THEET	thermoanaer
22	213	7.6	470	2	Q3CGY6_THEET	thermoanaer
23	213	7.6	470	2	Q97DG3_CLOAB	clostridium
24	212	7.6	468	2	Q8A412_BACTN	bacteroides
25	211.5	7.6	470	2	Q3CK48_THEET	thermoanaer
26	211.5	7.6	470	2	Q3CJR9_THEET	thermoanaer
27	211	7.6	470	2	Q3CEU2_THEET	thermoanaer
28	210.5	7.5	412	2	Q75TM9_9BACI	bacillus ho
29	210	7.5	470	2	Q3CJJ1_THEET	thermoanaer
30	209	7.5	469	2	Q420Q7_DESHA	desulfitoba
31	208.5	7.5	470	2	Q3CER4_THEET	thermoanaer
32	205.5	7.4	418	2	Q9KG88_BACHD	bacillus ha
33	205.5	7.4	423	2	Q4JCS6_LACRE	lactobacill
34	205.5	7.4	604	2	O73ZQ3_BACC1	bacillus ce
35	205	7.3	418	2	Q75TR9_BACHD	bacillus ha
36	204.5	7.3	418	2	Q75TN1_BACAG	bacillus ag
37	204.5	7.3	412	2	Q75TN4_9BACI	bacillus cl
38	204.5	7.3	412	2	Q75TN5_BACFI	bacillus fi
39	204.5	7.3	418	2	Q75TR8_BACHD	bacillus ha
40	204.5	7.3	418	2	Q9JWR9_BACHD	bacillus ha
41	204	7.3	434	2	Q74AB9_GEOSL	geobacter s
42	203.5	7.3	418	2	Q75TM8_9BACI	bacillus cl
43	203.5	7.3	418	2	Q75TN2_BACCS	bacillus ha
44	203.5	7.3	418	2	Q75TS2_BACHD	bacillus ha
45	198.5	7.1	627	2	Q74P60_BACC1	bacillus ce

ALIGNMENTS

```
RESULT 1
Q9XNK5_FUSOX
ID   Q9XNK5_FUSOX   PRELIMINARY;   PRT;   527 AA.
AC   Q9XNK5;
DT   01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Reverse transcriptase.
OS   Fusarium oxysporum f. sp. raphani.
OG   Mitochondrion.
OG   Plasmid pFOXC2.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
OC   Fusarium oxysporum complex.
OX   NCBI_TaxID=96318;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=699;
RX   MEDLINE=99417962; PubMed=10488338; DOI=10.1016/S1097-2765(00)80370-6;
RA   Walther T.C., Kennell J.C.;
RT   "Linear mitochondrial plasmids of F. oxysporum are novel, telomere-
RT   like retroelements.";
RL   Mol. Cell 4:229-238(1999).
CC   -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC   -------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -------------------------------------------------------------------------
DR   EMBL; AF124843; AAD38503.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR   InterPro; IPR000477; RVT.
DR   Pfam; PF00078; RVT_1; 1.
DR   PROSITE; PS50878; RT_POL; 1.
KW   Mitochondrion; Plasmid; RNA-directed DNA polymerase
KW   RNA-dependent DNA polymerase.
SQ   SEQUENCE 527 AA; 62085 MW; 605F5EA92B341C65 CRC64;

Query Match            100.0%;  Score 2790;  DB 2;  Length 527;
Best Local Similarity  100.0%;
Matches  527;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MNQISKNDSLDVLQDEMGQOKKTFESERKSLSGWDYFKSLGSIGRLPHFSRGIELREVKKA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MNQISKNDSLDVLQDEMGQOKKTFESERKSLSGWDYFKSLGSIGRLPHFSRGIELREVKKA 60

Qy   61 NRYLAFQEQRIVSAIEAGEIRKAVLVWLCLMKVSRSYQILLFNRVCKGWYWRWSTARVEE 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NRYLAFQEQRIVSAIEAGEIRKAVLVWLCLMKVSRSYQILLFNRVCKGWYWRWSTARVEE 120

Qy  121 IIFGAMNKMRSWDMKLLIHRFYILLKGNGKRPIGAPNYESRMISKALTDMLYSITEKSRS 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 IIFGAMNKMRSWDMKLLIHRFYILLKGNGKRPIGAPNYESRMISKALTDMLYSITEKSRS 180
```

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:26:26 ; Search time 192 Seconds
                                    (without alignments)
                                    1254.964 Million cell updates/sec

Title: US-10-765-456-1
Perfect score: 2790
Sequence: 1 MNQISKNDSLDVLQDEMGQK..........YWEIMQFHNLKRQQLRAIIE 527

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_8:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*
                10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2790	100.0	527	8	ADR14865	Adr14865 F. oxyspo
2	2550	91.4	527	8	ADR14866	Adr14866 F. oxyspo
3	227.5	8.2	439	6	ABP26156	Abp26156 Streptoco
4	212.5	7.6	420	6	ADB06930	Adb06930 Allococo
5	212.5	7.6	420	6	ADB06372	Adb06372 Allococo
6	212.5	7.6	420	6	ADB06624	Adb06624 Allococo
7	212.5	7.6	420	6	ADB10944	Adb10944 Allococo
8	212.5	7.6	420	6	ADB12629	Adb12629 Allococo
9	212.5	7.6	431	6	ADB06932	Adb06932 Allococo
10	212.5	7.6	431	6	ADB06374	Adb06374 Allococo
11	212.5	7.6	431	6	ADB10942	Adb10942 Allococo
12	212.5	7.6	431	6	ADB07658	Adb07658 Allococo
13	212.5	7.6	431	6	ADB09671	Adb09671 Allococo
14	212.5	7.6	431	6	ADB09679	Adb09679 Allococo
15	212.5	7.6	431	6	ADB12627	Adb12627 Allococo
16	212.5	7.6	431	6	ADB06626	Adb06626 Allococo
17	210.5	7.5	420	6	ADB06918	Adb06918 Allococo
18	210.5	7.5	431	6	ADB06920	Adb06920 Allococo
19	207.5	7.4	449	6	AED01456	Aed01456 C. acetob
20	194	7.0	425	5	ABP30367	Abp30367 Streptoco
21	194	7.0	436	5	ABP28457	Abp28457 Streptoco
22	192	6.9	395	9	AED01455	Aed01455 B. halodu
23	189.5	6.8	628	9	ADV16529	Adv16529 E. faecal
24	185	6.6	420	9	AED01445	Aed01445 G. stearo
25	185	6.6	455	9	AED01451	Aed01451 G. stearo
26	180	6.5	506	6	ABU33605	Abu33605 Protein e
27	178.5	6.4	599	2	AAW63835	Aaw63835 Lactococc
28	178.5	6.4	599	2	AAW81974	Aaw81974 Lactococc
29	178.5	6.4	599	2	AAY29984	Aay29984 Lactococc
30	178.5	6.4	599	3	AAY58019	Aay58019 Group II
31	172	6.2	496	7	ABO64657	Abo64657 Klebsiell
32	171	6.1	638	7	ADC94292	Adc94292 E. faeciu
33	168.5	6.0	605	7	ABO72234	Abo72234 Pseudomon
34	162	5.8	479	6	ABM70135	Abm70135 Photorhab
35	153.5	5.5	449	9	AED01457	Aed01457 Pseudomon
36	148.5	5.3	824	4	ABG10260	Abg10260 Novel hum
37	148	5.3	565	7	ABO68712	Abo68712 Pseudomon
38	148	5.3	3207	4	ABG10131	Abg10131 Novel hum
39	147	5.2	574	7	ABO68655	Abo68655 Pseudomon
40	146	5.2	1426	4	ABG11978	Abg11978 Novel hum
41	145	5.1	913	4	ABG02186	Abg02186 Novel hum
42	142.5	5.1	913	4	ABG14899	Abg14899 Novel hum
43	142.5	5.1	1144	4	ABG23203	Abg23203 Novel hum
44	141.5	5.0	832	8	ADH22665	Adh22665 Example P
45	138	4.9	514	4	ABG04464	Abg04464 Novel hum

ALIGNMENTS

RESULT 1
ID   ADR14865
AC   ADR14865 standard; protein; 527 AA.
XX
DT   04-NOV-2004 (first entry)
XX
DE   F. oxysporum reverse transcriptase from pFOXC2.
XX
KW   Reverse transcriptase; RT; pFOXC2; pFOXC3; 3' mismatch; cDNA synthesis;
KW   small RNA; small interfering RNA; RNA interference; gene silencing;
KW   siRNA.
XX
OS   Fusarium oxysporum.
XX
PN   US2004157213-A1.
XX
PD   12-AUG-2004.
XX
PF   26-JAN-2004; 2004US-00765456.
XX
PR   27-JAN-2003; 2003US-0442885P.
PR   02-APR-2003; 2003US-0459775P.
XX
PA   (KENN/) KENNELL J C.
XX
PI   Kennell JC;
XX
PT   New isolated fungal reverse transcriptases with enhanced capabilities,
PT   and encoding nucleic acid molecules, useful for research and diagnostic
PT   applications.
XX
PS   Claim 1; SEQ ID NO 1; 35pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a sequence
CC   that encodes a reverse transcriptase polypeptide or a fragment of a
CC   reverse transcriptase polypeptide comprising a sequence having 88%
CC   identity to ADR14865 or ADR14866, the reverse transcriptases encoded by
CC   Fusarium oxysporum plasmids pFOXC2 and pFOXC3. Also included are
CC   recombinant vector comprising a polynucleotide sequence (encoding the
CC   reverse transcriptases) appearing as ADR14867-ADR14870, a cell comprising
CC   an isolated polynucleotide that encodes a pFOXC-RT, making a pFOXC-RT

OM protein - protein search, using sw model

```
                    GenCore version 5.1.9
          Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:   July 11, 2006, 08:47:17 ; Search time 185 Seconds
                                     (without alignments)
                                     1319.536 Million cell updates/sec
Title:          US-10-765-456-1
Perfect score:  2790
Sequence:       1 MNQISKNDSLDVLQDEMGQK.........YWEIMQFHNLKRQQLRAIIE 527

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:    2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications AA Main:
  1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
  2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
  3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
  4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
  5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
  6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2790	100.0	527	4	US-10-765-456-1	Sequence 1, Appli
2	2550	91.4	527	4	US-10-765-456-2	Sequence 2, Appli
3	212.5	7.6	420	5	US-10-501-282-312	Sequence 312, App
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5	212.5	7.6	420	5	US-10-501-282-870	Sequence 870, App
6	212.5	7.6	420	5	US-10-501-282-4116	Sequence 4116, Ap
7	212.5	7.6	420	5	US-10-501-282-6084	Sequence 6084, Ap
8	212.5	7.6	431	5	US-10-501-282-314	Sequence 314, App
9	212.5	7.6	431	5	US-10-501-282-566	Sequence 566, App
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11	212.5	7.6	431	5	US-10-501-282-1598	Sequence 1598, Ap
12	212.5	7.6	431	5	US-10-501-282-3944	Sequence 3944, Ap
13	212.5	7.6	431	5	US-10-501-282-3952	Sequence 3952, Ap
14	212.5	7.6	431	5	US-10-501-282-4118	Sequence 4118, Ap
15	212.5	7.6	431	5	US-10-501-282-6086	Sequence 6086, Ap
16	210.5	7.5	420	5	US-10-501-282-858	Sequence 858, App
17	210.5	7.5	431	5	US-10-501-282-860	Sequence 860, App
18	185.5	6.6	599	4	US-10-008-618-6	Sequence 6, Appli
19	180	6.5	506	4	US-10-282-122A-61529	Sequence 61529, A
20	175.5	6.3	588	4	US-10-156-761-7777	Sequence 7777, Ap
21	167.5	6.0	627	6	US-11-079-463-6971	Sequence 6971, Ap
22	148.5	5.3	824	5	US-10-450-763-40619	Sequence 40619, A
23	147	5.2	3207	5	US-10-450-763-42337	Sequence 42337, A
24	145	5.2	1426	5	US-10-450-763-40490	Sequence 40490, A
25	142.5	5.1	913	5	US-10-450-763-32545	Sequence 32545, A
26	142.5	5.1	913	5	US-10-450-763-45258	Sequence 45258, A
27	141.5	5.1	1144	5	US-10-450-763-53562	Sequence 53562, A
28	141	5.1	761	6	US-11-079-463-5439	Sequence 5439, Ap
29	138	4.9	514	5	US-10-450-763-34823	Sequence 34823, A
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42	138	4.9	1307	5	US-10-450-763-40025	Sequence 40025, A
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ALIGNMENTS

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; Sequence 1, Application US/10765456
; Publication No. US20040157213A1
; GENERAL INFORMATION:
;   APPLICANT: Kennell, John C.
;   TITLE OF INVENTION: Fungal Reverse Transcriptases with Enhanced Capabilities
;   FILE REFERENCE: SLU02-010
;   CURRENT APPLICATION NUMBER: US/10/765,456
;   CURRENT FILING DATE: 2004-01-26
;   PRIOR APPLICATION NUMBER: 60/442,885
;   PRIOR FILING DATE: 2003-01-27
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: Microsoft Word 2000
; SEQ ID NO 1
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Fungal
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Qy        361 EGQSVSWDNPELEKWLKSINNLGYTKEPEWSWTVANGESFITKRKLNLTWMEIVKVVWFR 420
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Biocceleration Ltd.

GenCore version 5.1.9

Run on: July 11, 2006, 08:47:41 ; Search time 21 Seconds
673.357 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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8	97.5	3.5	723	7	US-11-174-307B-4990	Sequence 4990, Ap
9	95.5	3.4	749	7	US-11-312-958-62	Sequence 62, Appl
10	94	3.4	683	6	US-10-449-902-37410	Sequence 37410, A
11	94	3.4	683	6	US-10-449-902-43967	Sequence 43967, A
12	94	3.4	1016	6	US-10-449-902-43402	Sequence 43402, A
13	94	3.4	1315	6	US-10-527-411-141	Sequence 141, App
14	94	3.4	766	6	US-10-449-902-44105	Sequence 44105, A
15	93	3.3	447	6	US-10-953-349-10466	Sequence 10466, A
16	92.5	3.3	453	6	US-10-953-349-10465	Sequence 10465, A
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19	91.5	3.3	842	6	US-10-449-902-50282	Sequence 50282, A
20	91	3.3	632	6	US-11-245-628-21	Sequence 21, Appl
21	91	3.3	695	7	US-11-293-697-3799	Sequence 3799, Ap
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25	90	3.2	609	6	US-10-449-902-45540	Sequence 45540, A
26	90	3.2	609	6	US-10-449-902-45736	Sequence 45736, A
27	89.5	3.2	926	6	US-10-449-902-44353	Sequence 44353, A
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29	89	3.2	409	7	US-11-101-316-22	Sequence 22, Appl
30	89	3.2	479	6	US-10-471-571A-2982	Sequence 2982, Ap
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45	87.5	3.1	1066	6	US-10-521-401A-13	Sequence 13, Appl

ALIGNMENTS

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; Sequence 4159, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4159
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4159

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Best Local Similarity 21.7%; Pred. No. 0.34;
Matches 60; Conservative 53; Mismatches 98; Indels 66; Gaps 14;

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; Sequence 56343, Application US/10449902

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID		Description
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3	227.5	8.2	439	34	US-10-415-182A-1488	Sequence 1488, Ap
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23	212.5	7.6	431	1	PCT-US02-36123-4116	Sequence 4116, Ap
24	212.5	7.6	431	1	PCT-US02-36123-3952	Sequence 3952, Ap
25	212.5	7.6	431	1	PCT-US02-36123-3944	Sequence 3944, Ap
26	212.5	7.6	431	1	PCT-US02-36123-1598	Sequence 1598, Ap
27	212.5	7.6	431	35	US-10-501-282-872	Sequence 872, App
28	212.5	7.6	431	35	US-10-501-282-566	Sequence 566, App
29	212.5	7.6	431	35	US-10-501-282-314	Sequence 314, App
30	210.5	7.5	420	1	PCT-US02-36123-858	Sequence 858, App
31	210.5	7.5	431	35	US-10-501-282-858	Sequence 858, App
32	210.5	7.5	420	1	PCT-US02-36123-860	Sequence 860, App
33	210.5	7.5	431	35	US-10-501-282-860	Sequence 860, App
34	210.5	7.5	431	34	US-10-415-182A-9910	Sequence 9910, App
35	194	7.0	436	34	US-10-415-182A-6090	Sequence 6090, App
36	194	7.0	425	34	US-09-252-691-6535	Sequence 6535, Ap
37	190.5	6.8	467	22	US-09-252-691C-6535	Sequence 6535, Ap
38	190.5	6.8	467	22	US-10-417-886-6535	Sequence 6535, Ap
39	190.5	6.8	467	34	US-10-558-119-224	Sequence 224, App
40	189.5	6.7	628	35	PCT-US99-04404-6	Sequence 6, Appli
41	187.5	6.7	599	30	US-10-008-618-6	Sequence 6, Appli
42	185.5	6.6	599	30	US-10-797-262-2	Sequence 2, Appli
43	185	6.6	420	37	US-10-797-262-8	Sequence 8, Appli
44	180	6.5	506	1	US-10-282-09107B-61529	Sequence 61529, A
45	180	6.5	506	32	US-10-282-122A-61529	Sequence 61529, A

ALIGNMENTS

RESULT 1
US-10-765-456-1
; US-10-765-456-1
; Sequence 1, Application US/10765456
; GENERAL INFORMATION:

OM protein - protein search, using sw model

GenCore version 5.1.9

Run on: July 11, 2006, 08:36:56 ; Search time 25 Seconds
(without alignments)
905.259 Million cell updates/sec

Title: US-10-765-456-1
Perfect score: 2790
Sequence: 1 MNQISKNDSLDVLQDEMQQK..........YWEIMQFHNLKRQQLRAIIE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 193904 seqs, 42943980 residues

Total number of hits satisfying chosen parameters: 193904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database :   Pending_Patents_AA_New:*
1: /EMC_Celerra_SIDS3/ptcdata/1/paa/PCT_NEW_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptcdata/1/paa/US06_NEW_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptcdata/1/paa/US07_NEW_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptcdata/1/paa/US08_NEW_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptcdata/1/paa/US09_NEW_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptcdata/1/paa/US10_NEW_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptcdata/1/paa/US11_NEW_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptcdata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	227.5	8.2	439	7	US-11-434-137-1488	Sequence 1488, Ap
2	227.5	8.2	439	7	US-11-434-184-1488	Sequence 1488, Ap
3	227.5	8.2	439	7	US-11-434-127-1488	Sequence 1488, Ap
4	227.5	8.2	439	7	US-11-434-199-1488	Sequence 1488, Ap
5	227.5	8.2	439	7	US-11-434-203-1488	Sequence 1488, Ap
6	194	7.0	425	7	US-11-434-184-9910	Sequence 9910, Ap
7	194	7.0	425	7	US-11-434-137-9910	Sequence 9910, Ap
8	194	7.0	425	7	US-11-434-203-9910	Sequence 9910, Ap
9	194	7.0	425	7	US-11-434-127-9910	Sequence 9910, Ap
10	194	7.0	425	7	US-11-434-199-9910	Sequence 9910, Ap
11	194	7.0	436	7	US-11-434-184-6090	Sequence 6090, Ap
12	194	7.0	436	7	US-11-434-203-6090	Sequence 6090, Ap
13	194	7.0	436	7	US-11-434-127-6090	Sequence 6090, Ap
14	194	7.0	436	7	US-11-434-199-6090	Sequence 6090, Ap
15	194	7.0	436	7	US-11-434-137-6090	Sequence 6090, Ap
16	136	4.9	330	7	US-11-027-891A-4317	Sequence 4317, Ap
17	136	4.9	330	7	US-11-027-879A-4317	Sequence 4317, Ap
18	112	4.0	861	7	US-11-437-729-1739	Sequence 1739, Ap
19	112	4.0	1121	7	US-11-437-729-1736	Sequence 1736, Ap
20	112	4.0	2427	7	US-11-437-729-1733	Sequence 1733, Ap
21	112	4.0	2432	7	US-11-437-729-1731	Sequence 1731, Ap
22	112	4.0	2438	7	US-11-437-729-1740	Sequence 1740, Ap
23	112	4.0	2452	7	US-11-437-729-1734	Sequence 1734, Ap
24	112	4.0	2452	7	US-11-437-729-1738	Sequence 1738, Ap
25	112	4.0	2472	7	US-11-437-729-1735	Sequence 1735, Ap
26	112	4.0	2472	7	US-11-437-729-1737	Sequence 1737, Ap
27	112	4.0	2480	7	US-11-437-729-1732	Sequence 1732, Ap
28	111	4.0	456	7	US-11-357-421-235	Sequence 235, App
29	110.5	4.0	570	7	US-11-431-855-7999	Sequence 7999, App
30	108.5	3.9	623	7	US-11-027-891A-4292	Sequence 4292, Ap
31	108.5	3.9	623	7	US-11-027-879A-4292	Sequence 4292, Ap
32	102.5	3.7	509	6	US-10-943-507A-194	Sequence 194, Appl
33	101	3.6	316	4	US-08-808-031B-45	Sequence 45, Appl
34	100.5	3.6	509	7	US-10-943-507A-268	Sequence 268, App
35	99.5	3.6	509	6	US-10-943-507A-260	Sequence 260, App
36	95.5	3.4	427	7	US-11-431-855-15561	Sequence 15561, A
37	95	3.4	737	7	US-11-431-855-26091	Sequence 26091, A
38	95	3.4	737	1	PCT-US06-17161-188	Sequence 188, App
39	93.5	3.4	398	1	PCT-US06-17161-189	Sequence 189, App
40	93.5	3.4	475	7	US-11-431-855-9060	Sequence 9060, Ap
41	93	3.3	475	7	PCT-US06-03007A-19	Sequence 19, Appl
42	93	3.3	774	5	US-11-431-855-40	Sequence 40, Appl
43	93	3.3	427	4	US-08-808-0318-40	Sequence 40, Appl
44	92.5	3.3	427	1	PCT-US06-03007A-19	Sequence 19, Appl
45	92.5	3.3	509	6	US-10-943-507A-563	Sequence 563, App

ALIGNMENTS

RESULT 1
US-11-434-137-1488
Sequence 1488, Application US/11434137
GENERAL INFORMATION:
APPLICANT: Telford, John
APPLICANT: Masignani, Vega
APPLICANT: Ros, Immaculada Margarit Y
APPLICANT: Fraser, Claire
APPLICANT: Tettelin, Herve
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/11/434,137
CURRENT FILING DATE: 2006-05-16
PRIOR APPLICATION NUMBER: US 10/415,182
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: PCT/GB01/04789
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: GB-0026333.5
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: GB-0028727.6
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: GB-0105640.7
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 12025
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 1488
LENGTH: 439
TYPE: PRT
ORGANISM: Streptococcus agalactiae

US-11-434-137-1488

Query Match 8.2%;   Score 227.5;   DB 7;   Length 439;
Best Local Similarity 24.9%;   Pred. No. 5.7e-10;
Matches 87;   Conservative 53;   Mismatches 114;   Indels 95;   Gaps 15;

```
Qy  138 IHRFYILKKNGKMRPIGAPNYESRMISKALTDMLYSITEKSRSAEOHGYMKKRGAWSAIL 197
            :  ||| ||||  :||:: | |:  :  ||: :: ||: ::
Db   95 VRRVYIPKANGKKRPLGIPTVRDRVVQTAVKIVIEPIFEADFQEFSYGFRPKRSANQAIR 154

Qy  198 ECLSKLKEGYAG-YEPDLKSFNTV--EPFIYFRKLEEVDKKLTKLISNVIKGIEYRFSE 254
         | |||  | || : |:|:| | :|:|:
Db  155 EIYKYLNYGCEWVIDADLKGYPDTIPHDKLLLVKERVTDKSIIKLLSIWLE------AG 208

Qy  255 LLPESELNPKANRKNTLERTGVPQGLSLSPLLST------------W---ALEYGRPENLIM 302
         :|  :|:  ||
Db  209 IMEDNQV------RSNIL---GTPQGGVISPLLANIYLNALDRYWKNNRLEGRGHDAHLIR 260

Qy  303 YADDGIYFFKHNISKFTRWI-ERMGRAGIEISPEKSGSL--TPVFKFCGVTIDQPK---- 355
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OM nucleic - nucleic search, using sw model

```
                                   GenCore version 5.1.9
                      Copyright (c) 1993 - 2006  Bioacceleration Ltd.
```

Run on: July 11, 2006, 06:46:21 ; Search time 8843 Seconds
                                            (without alignments)
                                            11454.565 Million cell updates/sec

Title: US-10-765-456-3
Perfect score: 1584
Sequence: 1 atgaatcaaatctctaaaaa.........tcagggctataattgagtag 1584

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 6366136 seqs, 319737105225 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1564.8 | 98.8 | 1905 | 4 | AF124843 | AF124843 Fusarium |
| 2 | 1543.2 | 97.4 | 1726 | 4 | AF005241 | AF005241 Fusarium |
| 3 | 1185.6 | 74.8 | 1836 | 4 | AF124844 | AF124844 Fusarium |
| 4 | 68.2 | 4.3 | 7218 | 2 | I66494 | I66494 Sequence 14 |
| 5 | 64.4 | 4.1 | 785 | 2 | AF005240 | AF005240 Fusarium |
| 6 | 50.8 | 3.2 | 2000 | 2 | AX655393 | AX655393 Sequence |
| 7 | 48.4 | 3.1 | 14461 | 2 | AX256438 | AX256438 Sequence |
| 8 | 48.2 | 3.0 | 2000 | 2 | AX655393 | AX655393 Sequence |
| 9 | 46.2 | 2.9 | 335050 | 13 | PPA929356 | AL929356 Plasmodiu |
| 10 | 45.8 | 2.9 | 104492 | 12 | AC023358 | AC023358 Homo sapi |
| 11 | 45.8 | 2.9 | 157097 | 12 | AC027784 | AC027784 Homo sapi |
| 12 | 45.8 | 2.9 | 184864 | 5 | AC018927 | AC018927 Homo sapi |
| 13 | 45.4 | 2.9 | 2000 | 4 | AX508575 | AX508575 Sequence |
| 14 | 45.4 | 2.9 | 84723 | 4 | AC010675 | AC010675 Arabidops |
| 15 | 44.8 | 2.8 | 114505 | 4 | F20P5 | AC002062 Sequence |
| 16 | 44.8 | 2.8 | 147079 | 5 | AL772262 | AL772262 Human DNA |
| 17 | 44.6 | 2.8 | 2822 | 5 | AB169417 | AB169417 Macaca fa |
| 18 | 44 | 2.8 | 164834 | 6 | AL929043 | AL929043 Mouse DNA |
| 19 | 44 | 2.8 | 209762 | 6 | AC114822 | AC114822 Mus muscu |
| 20 | 43.8 | 2.8 | 194562 | 12 | AC174219 | AC174219 Bos tauru |
| 21 | 43.8 | 2.8 | 266757 | 12 | AC152522 | AC152522 Bos tauru |
| 22 | 43.6 | 2.8 | 154485 | 12 | AC079056 | AC079056 Homo sapi |
| 23 | 43.6 | 2.8 | 179929 | 5 | AC006270 | AC006270 Homo sapi |
| 24 | 43.6 | 2.8 | 181716 | 12 | AC068285 | AC068285 Homo sapi |
| 25 | 43.4 | 2.7 | 212412 | 12 | AC173526 | AC173526 Bos tauru |
| 26 | 43.2 | 2.7 | 100953 | 5 | AC009489 | AC009489 Homo sapi |
| 27 | 43.2 | 2.7 | 115863 | 5 | HSU537P22 | HSU537P22 Homo sapi |
| 28 | 43.2 | 2.7 | 192272 | 12 | AC181686 | AC181686 Strongylo |
| 29 | 43.2 | 2.7 | 306749 | 5 | CNS07EP9 | CNS07EP9 Homo sapi |
| 30 | 43.2 | 2.7 | 73565 | 5 | AL590310 | AL590310 Homo sapi |
| 31 | 43.0 | 2.7 | 157065 | 12 | AC067962 | AC067962 Homo sapi |
| 32 | 42.8 | 2.7 | 171849 | 12 | AC175179 | AC175179 Homo sapi |
| 33 | 42.8 | 2.7 | 213849 | 12 | AC149749 | AC149749 Bos tauru |
| 34 | 42.8 | 2.7 | 249292 | 12 | AC151082 | AC151082 Homo sapi |
| 35 | 42.6 | 2.7 | 171718 | 12 | AC022501 | AC022501 Homo sapi |
| 36 | 42.6 | 2.7 | 175069 | 12 | AC164693 | AC164693 Bos tauru |
| 37 | 42.4 | 2.7 | 156794 | 12 | CT027830 | CT027830 Danio rer |
| 38 | 42.4 | 2.7 | 173690 | 11 | BX465211 | BX465211 Zebrafish |
| 39 | 42.4 | 2.7 | 202612 | 12 | CR848046 | CR848046 Danio rer |
| 40 | 42.2 | 2.7 | 164455 | 5 | AL161897 | AL161897 Human DNA |
| 41 | 42.2 | 2.7 | 161593 | 5 | HSBA49G10 | AL121901 Human DNA |
| 42 | 42.2 | 2.7 | 174413 | 12 | AC011788 | AC011788 Homo sapi |
| 43 | 42.2 | 2.7 | 191120 | 12 | AC163486 | AC163486 Mus muscu |
| 44 | 42.2 | 2.7 | 208992 | 6 | AC153881 | AC153881 Mus muscu |
| 45 | 42.2 | 2.7 | 211591 | 12 | AC160717 | AC160717 Bos tauru |

ALIGNMENTS

```
RESULT 1
AF124843
LOCUS       AF124843              1905 bp    DNA     linear   PLN 02-JUL-2003
DEFINITION  Fusarium oxysporum f. sp. raphani mitochondrial plasmid pFOXC2,
            complete sequence.
ACCESSION   AF124843
VERSION     AF124843.1  GI:5052323
KEYWORDS    .
SOURCE      mitochondrion Fusarium oxysporum f. sp. raphani
  ORGANISM  Fusarium oxysporum f. sp. raphani
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreales; Nectriaceae; Fusarium;
            Fusarium oxysporum complex.
REFERENCE   1  (bases 1 to 1905)
  AUTHORS   Walther,T.C. and Kennell,J.C.
  TITLE     Linear mitochondrial plasmids of F. oxysporum are novel,
            telomere-like retroelements
  JOURNAL   Mol. Cell 4 (2), 229-238 (1999)
  PUBMED    10488338
REFERENCE   2  (bases 1 to 1905)
  AUTHORS   Kennell,J.C. and Walther,T.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-1999) Biological Sciences, Southern Methodist
            University, 220 Fondren Science, Dallas, TX 75275-0376, USA
FEATURES             Location/Qualifiers
     source          1..1905
                     /organism="Fusarium oxysporum f. sp. raphani"
                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
                     /strain="699"
                     /db_xref="taxon:96318"
                     /plasmid="pFOXC2"
                     /note="forma specialis: raphani"
                     /forma_specialis: raphani"
     CDS             272..1855
                     /codon_start=1
                     /transl_table=4
                     /product="reverse transcriptase"
                     /protein_id="AAD38503.1"
                     /db_xref="GI:5052324"
                     /translation="MNQISKNDSLDVLQDEMGQKKTFESERKSLSGWDYFKSLGSIGR
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: July 11, 2006, 06:46:35 ; Search time 7954 Seconds
(without alignments)
11136.060 Million cell updates/sec

Title: US-10-765-456-3
Perfect score: 1584
Sequence: 1 atgaatcaaatctctcaaaaa..........tcagggctataattgagtag 1584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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1:  gb_est1:*
2:  gb_est3:*
3:  gb_est4:*
4:  gb_est5:*
5:  gb_est6:*
6:  gb_htc:*
7:  gb_est2:*
8:  gb_est7:*
9:  gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87.6	5.5	281	10	DW177370	DW177370 DD59 Fusa
c 2	57.6	3.6	997	14	CNS005TE	AL060767 Drosophil
c 3	50.8	3.2	1687	1	AM090701	AM090701 AM090701
c 4	50.4	3.1	1101	14	CNS0039G	AL063921 Drosophil
c 5	48.8	3.1	1101	14	CNS012VN	AL102077 Drosophil
c 6	47.2	3.0	1050	14	CNS012VN	AG133232 Drosophil
c 7	47.2	3.0	1101	14	CNS0006J	AG062049 Drosophil
c 8	47	3.0	956	14	CT070073	CT070073 Sus scrof
c 9	47	3.0	1007	14	CNS00JOV	CT070073 Drosophil
c 10	46	2.9	1101	14	CNS0106X	AL076752 Drosophil
c 11	45.8	2.9	828	14	CNS011TX	AL098595 Drosophil
c 12	45.4	2.9	1101	14	CNS000D1	AL100719 Drosophil
c 13	44.8	2.8	684	11	BZ433974	AL065414 Drosophil
c 14	44.8	2.8	777	11	BZ071235	BZ433974 BONOS76TF
c 15	44.8	2.8	786	11	BH938760	BZ071235 1kg56d07.
c 16	44.8	2.8	1342	10	DV781885	BH938760 cdg13b10.
c 17	44.4	2.8	742	14	AG469000	DV781885 Hw_FAT_17
c 18	44.4	2.8	839	14	DU959126	AG469000 Mus muscu
c 19	44.4	2.8	1204	14	CNS016E2	DU959126 229868 TO
c 20	44	2.8	616	14	CNS006LZ	AL065735 Drosophil
c 21	43.8	2.8	657	13	CZ926091	CZ926091 109842212
c 22	43.8	2.8	756	13	DU270450	DU270450 109838000
c 23	43.8	2.8	888	14	CNS02C98	AL190853 Tetraodon
c 24	43.8	2.8	1474	12	CG749456	CG749456 P043-3-G0
c 25	43.2	2.7	501	12	CC965772	CC965772 BOIFB18TR
c 26	43.2	2.7	605	11	BH704585	BH704585 BOHVD1STR
c 27	43.2	2.7	653	11	BH685525	BH685525 BOMEA53TF
c 28	43.2	2.7	667	13	BH533961	BH533961 BOCIG69TF
c 29	43.2	2.7	667	11	BH538544	BH538544 BOHLT6TR
c 30	43.2	2.7	683	11	BH992999	BH992999 oeh28g12.
c 31	43.2	2.7	691	11	BH946440	BH946440 obu8bb10.
c 32	43.2	2.7	697	11	BH961943	BH961943 obu97b09.
c 33	43.2	2.7	704	11	BZ055027	BZ055027 jnr31b06.
c 34	43.2	2.7	721	11	BH972815	BH972815 odd62d10.
c 35	43.2	2.7	731	11	BOHWV93TF	BOHWV93TF odd62d10.
c 36	43.2	2.7	740	11	BH714645	BH714645 1l998f03.
c 37	43.2	2.7	753	11	BZ060417	BZ060417 1l998f03.
c 38	43.2	2.7	756	11	BH688650	BH688650 1k267d10.
c 39	43.2	2.7	760	11	BH688650	BOMF96TR.
c 40	43.2	2.7	760	12	CC943672	BH421764 BOHNV9TF
c 41	43.2	2.7	822	11	BH655342	CC943672 BOICS80TR
c 42	43.2	2.7	825	11	BH501985	BH655342 BOMIE43TF
c 43	43.2	2.7	825	11	BH498276	BH501985 BOGGC94TR
c 44	43.2	2.7	840	11	BZ460099	BH498276 BOGWA29TF
c 45	43.2	2.7	1054	11	BZ504662	BZ460099 BONKQ6STR
			1054	11		BZ504662 BONIJ13TR

ALIGNMENTS

RESULT 1
DW177370

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LOCUS       DW177370                 281 bp    mRNA    linear    EST 29-DEC-2005
DEFINITION  DD59 Fusarium culmorum Differential Display library Fusarium
            culmorum cDNA, mRNA sequence.
ACCESSION   DW177370
VERSION     DW177370.1  GI:84067500
KEYWORDS    EST.
SOURCE      Fusarium culmorum
  ORGANISM  Fusarium culmorum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE   1  (bases 1 to 281)
  AUTHORS   Lysoe,E., Bone,K. and Klemsdal,S.
  TITLE     Differential Display RT-PCR in high zearalenone producing strains
            of Fusarium
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Lysoe E
            Bioforsk Plantehelse
            Genetics and biotechnology
            Hogskoleveien 7, 1432 Aas, Norway
            Tel: +47 69949252
            Fax: +47 64947110
            Email: erik.lysoe@bioforsk.no.
FEATURES             Location/Qualifiers
     source          1..281
                     /organism="Fusarium culmorum"
                     /mol_type="mRNA"
                     /db_xref="taxon:5516"
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                     library"
ORIGIN
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Query Match 5.5%; Score 87.6; DB 10; Length 281;
Best Local Similarity 57.2%;
Matches 159; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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Qy    151 GGAATTGAATTACAGAGAGTCAAGAAAGCAAATAGATATCTTGCCTTCCAGGAGCAAAGG 210
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Db      2 GGGATTAAGTACTCTGACGTAGACGAGCAGAGCCAATAGGTATCTCACATTCCAGGAGTGA 61

Qy    211 ATTGTTAGCGCAATAGAAGCGGCGCAAAATCGTAAGGCAGTGCTAGTGTGGCTATGTTA 270
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                              GenCore version 5.1.9
                              Copyright (c) 1993 - 2006  Bioacceleration Ltd.

QM nucleic - nucleic search, using sw model

Run on:          July 11, 2006, 06:44:56 ; Search time 967 Seconds
                                           (without alignments)
                                           11420.932 Million cell updates/sec

Title:           US-10-765-456-3
Perfect score:   1584
Sequence:        1 atgatcaaatctctaaaaa..........tcagggctataattgagtag 1584
Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        5244920 seqs, 346124231 residues
Total number of hits satisfying chosen parameters:        10489840
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
                                                     %
Result                     Query
No.      Score   Match Length DB    ID            Description
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c 10       44.4    2.8   2000   11  ACL37108       Acl37108 Rice stre
c 11       42      2.7   2000   11  ACL35363       Acl35363 Rice stre
c 12       41.4    2.6   5798   6  ABL33666        Abl33666 Human imm
c 13       39.8    2.5   2064   8  ACA28930        Aca28930 Prokaryot
  14       39.6    39  101954  13  ABD33574        Abd33574 Human can
c 15       39      2.5  13345  13  AAK66901        Aak66901 Human imm
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c 18       38.2    2.4  11793  12  ADO03803        Ado03803 Human Cc1
c 19       38.2    2.4 156652  14  AEA61138        Aea61138 Human UGT
c 20       38      2.4 114633  11  ACN44332        Acn44332 Mouse gen
c 21       37.8    2.4   1395   5  AAS71385        Aas71385 DNA encod
c 22       37.8    2.4   3540   2  AAX06875        Aax06875 Yeast NPC
c 23       37.8    2.4   6815   4  AAS41927        Aas41927 Genomic s
  24       37.8    2.4   6815   10  ADC46543       Adc46543 Human neo
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c 26       37.6    2.4    324   6  ABL77477        Abl77477 Human ova
c 27       37.6    2.4  90183  12  ADQ97960_3      Continuation (4 of
c 28       37.6    2.4  95124  14  AEE04750        Aee04750 Cancer-as
c 29       37.4    2.4    544   2  AAX20396        Aax20396 Borrelia
  30       37.4    2.4    678  12  ADM91226        Adm91226 Human DNA
  31       37.4    2.4    678  12  ADM90808        Adm90808 Human DNA
  32       37.4    2.4    678  12  ADM90807        Adm90807 Human DNA
  33       37.4    2.4    678  12  ADM91225        Adm91225 Human DNA
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  36       37      2.3    517  11  ABA60603        Aba60603 Human foe
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                              ALIGNMENTS

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ADR14867

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DT   04-NOV-2004  (first entry)
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KW   Reverse transcriptase; RT; pFOXC2; pFOXC3; 3' mismatch; cDNA synthesis;
KW   small RNA; small interfering RNA; RNA interference; gene silencing;
KW   siRNA; ds.
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OS   Fusarium oxysporum.
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FH   Key             Location/Qualifiers
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PF   26-JAN-2004; 2004US-00765456.
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PR   27-JAN-2003; 2003US-0442885P.
PR   02-APR-2003; 2003US-0459775P.
XX
PA   (KENN/) KENNELL J C.
XX
PI   Kennell JC;
XX
PT   WPI; 2004-580263/56.
PT   P-PSDB; ADR14865.
XX
PT   New isolated fungal reverse transcriptases with enhanced capabilities,
PT   and encoding nucleic acid molecules, useful for research and diagnostic
PT   applications.
XX
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
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Run on: July 11, 2006, 06:49:55 ; Search time 1862 Seconds
                                            (without alignments)
                                            10453.069 Million cell updates/sec

Title: US-10-765-456-3
Perfect score: 1584
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 18892170 seqs, 614381763B residues
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1564.8	98.8	1905	8	US-10-765-456-5	Sequence 5, Appli
3	1204.8	76.1	1584	8	US-10-765-456-4	Sequence 4, Appli
4	1185.6	74.8	1836	8	US-10-765-456-6	Sequence 6, Appli
5	45.4	2.9	2000	3	US-09-938-842A-3270	Sequence 3270, Ap
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12	42.2	2.7	660	7	US-10-141-761-480	Sequence 480, App
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US-10-765-456-3
        Sequence 3, Application US/10765456
        Publication No. US20040157213A1

GENERAL INFORMATION:
        APPLICANT: Kennell, John C.
        TITLE OF INVENTION: Fungal Reverse Transcriptases with Enhanced Capabilities
        FILE REFERENCE: SLU02-010
        CURRENT APPLICATION NUMBER: US/10/765,456
        CURRENT FILING DATE: 2004-01-26
        PRIOR APPLICATION NUMBER: 60/442,885
        PRIOR FILING DATE: 2003-01-27
        NUMBER OF SEQ ID NOS: 39
        SOFTWARE: Microsoft Word 2000

SEQ ID NO 3
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        TYPE: DNA
        ORGANISM: fungal
US-10-765-456-3

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Best Local Similarity   100.0%; Pred. No. 0; Mismatches 0;
Matches 1584; Conservative 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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                        GenCore version 5.1.9
                Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:          July 11, 2006, 06:47:12 ; Search time 320 Seconds
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Title:           US-10-765-456-3
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Total number of hits satisfying chosen parameters:       2807332

Minimum DB seq length: 0
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                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.
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SUMMARIES

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ALIGNMENTS

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Sequence 14, Application US/0823463
Patent No. 5670367
GENERAL INFORMATION:
;  APPLICANT: DORNER, F.
;  APPLICANT: SCHIFLINGER, F.
;  APPLICANT: FALKNER, F. G.
;  TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;  NUMBER OF SEQUENCES: 52
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Foley & Lardner
;  STREET: 1800 Diagonal Road, Suite 500
;  CITY: Alexandria
;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22313-0299
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/232,463
;  FILING DATE:
;  CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US/07/935,313
;  FILING DATE:
;  APPLICATION NUMBER: EP 91 114 300.6
;  FILING DATE: 26-AUG-1991
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;  TELEX: 899149
;  TELEX: 89914
;  INFORMATION FOR SEQ ID NO: 14:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 7218 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  IMMEDIATE SOURCE:
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